

FIGURE 1

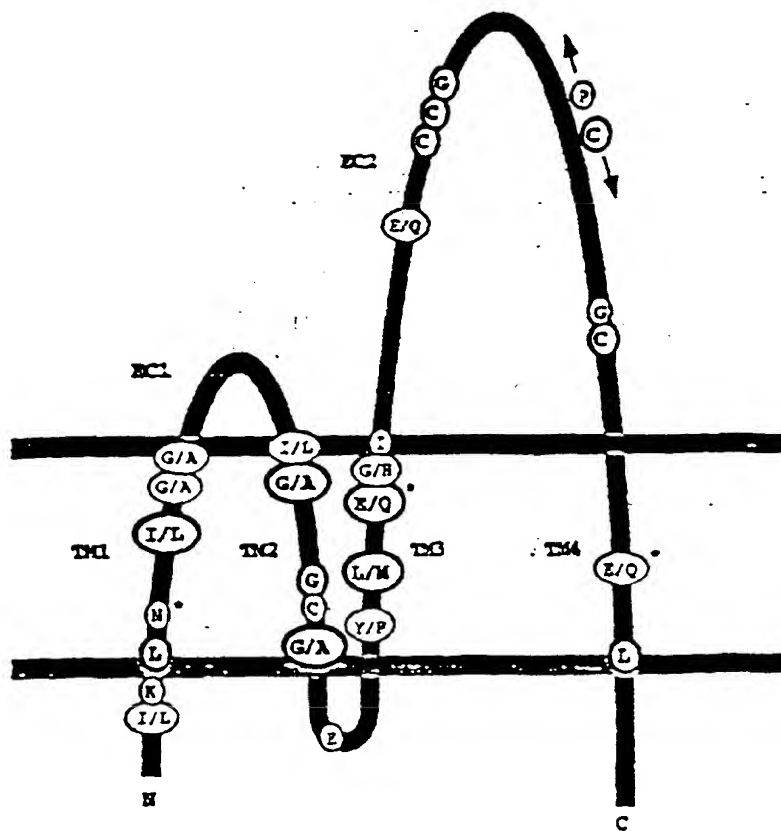


FIGURE 2A

```
1  CTTCTCGGC CGAGCCGGGC CGCGCGGCCG CTGCCGCCGC CGCGCGCGGA
   GAAGGAGCCG GCTCGGCCCC GCGCGCCGGC GACGGCGGGC GCGCGCGCCT

+1  ]-----
51  TTCTGCTTCT CAGAAGATGC ACTATTATAG ATACTCTAAC GCCAAGGTCA
   AAGACGAAGA GTCTTCTACG TGATAATATC TATGAGATTG CGGTTCCAGT

+1  -----
101 GCTGCTGGTA CAAGTACCTC CTTTTCAGCT ACAACATCAT CTTCTGGTTG
    CGACGACCAT GTTCATGGAG GAAAAGTCGA TGTGTAGTA GAAGACCAAC
-3  <-----

+3  ]-----
+1  -----
151 GCTGGAGTTG TCTTCCTTGG AGTCGGGCTG TGGGCATGGA GCGAAAAGGG
    CGACCTCAAC AGAAGGAACC TCAGCCCGAC ACCCGTACCT CGCTTTTCCC
-3  -----

+3  -----
+1  -----
201 TGTGCTGTCC GACCTCACCA AAGTGACCCG GATGCATGGA ATCGACCCTG
    ACACGACAGG CTGGAGTGGT TTCCTGGGC CTACGTACCT TAGCTGGGAC
-3  -----

+3  -----
+1  -----
251 TGGTGTGGT CCTGATGGTG GGCGTGGTGA TGTTACCCT GGGGTTGCGC
    ACCAGACCA GGACTACCAC CCGCACCCT ACAAGTGGGA CCCCAGCGG
-3  -----

+3  -----
+1  -----
301 GGCTGCGTGG GGGCTCTGCG GGAGAATATC TGCTTGCTCA ACTTTTCTG
    CCGACGCACC CCGGAGACGC CCTCTTATAG ACGAACGAGT TGAAAAAGAC
-3  -----

+3  -----
+1  -----
351 TGGCACCATC GTGCTCATCT TCTTCCTGGA GCTGGCTGTG GCCGTGCTGG
    ACCGTGGTAG CACGAGTAGA AGAAGGACCT CGACCGACAC CGGCACGACC
-3  -----

+3  -----
+1  -----
401 CTTCTCTGTT CCAGGACTGG GTGAGGGACC GGTCCGGGA GTTCTTCGAG
    GGAAGGACAA GGTCTGACC CACTCCCTGG CCAAGGCCCT CAAGAAGCTC
-3  -----

+3  -----
+1  -----
                               ClaI
                               ~~~~~
451 AGCAACATCA AGTCCTACCG GGACGATATC GATCTGCAAA ACCTCATCGA
    TCGTTGTAGT TCAGGATGGC CCTGCTATAG CTAGACGTTT TGGAGTAGCT
-3  -----[

+3  ----->
+1  -----
501 CTCCCTTCAG AAAGCTAACC AGTGCTGTGG CGCATATGGC CCTGAAGACT
    GAGGGAAGTC TTTCGATTGG TCACGACACC GCGTATACCG GGAATTCTGA
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FIGURE 2B

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+1 -----
551 GGGACCTCAA CGTCTACTTC AATTGCAGCG GTGCCAGCTA CAGCCGAGAG
    CCCTGGAGTT GCAGATGAAG TTAACGTCGC CACGGTCGAT GTCGGCTCTC

+1 -----
601 AAGTGCGGGG TCCCTTCTC CTGCTGCGTG CCAGATCCTG CGCAAAAAGT
    TTCACGCCCC AGGGGAAGAG GACGACGCAC GGTCTAGGAC GCGTTTTTCA

+1 -----
651 TGTGAACACA CAGTGTGGAT ATGATGTCAG GATTGAGCTG AAGAGCAAGT
    ACACTTGTGT GTCACACCTA TACTACAGTC CTAAGTCGAC TTCTCGTTCA

+1 -----
701 GGGATGAGTC CATCTTCACG AAAGGCTGCA TCCAGGCGCT GGAAAGCTGG
    CCCTACTCAG GTAGAAGTGC TTTCCGACGT AGGTCCGCGA CCTTTCGACC

+1 -----
751 CTCCCGCGGA ACATTTACAT TGTGGCTGGC GTCTTCATCG CCATCTCGCT
    GAGGGCGCCT TGTAATGTA ACACCGACCG CAGAAGTAGC GGTAGAGCGA
-1 -----

+1 -----
801 GTTGACAGATA TTTGGCATCT TCCTGGCAAG GACGCTGATC TCAGACATCG
    CAACGTCTAT AAACCGTAGA AGGACCGTTC CTGCGACTAG AGTCTGTAGC
-1 -----

+1 -----
851 AGGCAGTGAA GGCCGGCCAT CACTTCTGAG GAGCAGAGTT GAGGGAGCCG
    TCCGTCACCT CCGGCCGTA GTGAAGACTC CTCGTCTCAA CTCCCTCGGC
-1 -----

+1 -----
901 AGCTGAGCCA CGCTGGGAGG CCAGAGCCTT TCTCTGCCAT CAGCCCTACG
    TCGACTCGGT GCGACCTCC GGTCTCGGAA AGAGACGGTA GTCGGGATGC
-1 -----

+1 -----
951 TCCAGAGGGA GAGGAGCCGA CACCCCAGA GCCAGTGCCC CATCTTAAGC
    AGGTCTCCCT CTCCTCGGCT GTGGGGGTCT CGGTCACGGG GTAGAATTCG
-1 -----

+1 -----
1001 ATCAGCGTGA CGTGACCTCT CTGTTTCTGC TTGCTGGTGC TGAAGACCAA
    TAGTCGCACT GCACTGGAGA GACAAAGACG AACGACCACG ACTTCTGGTT

+1 -----
1051 GGGTCCCCCT TGTTACCTGC CCAAAGTGT GACTGCATCC CTCTGGAGTC
    CCCAGGGGGA ACAATGGACG GGTTTGAACA CTGACGTAGG GAGACCTCAG

+1 -----
1101 TACCCAGAGA CAGAGAATGT GTCTTTATGT GGGAGTNGTG ACTCTGAAAG
    ATGGGTCTCT GTCTTTACA CAGAAATACA CCCTCANCAC TGAGACTTTC
-1 -----

+1 -----
PstI
1151 ACAGAGAGGG CTCCTGTGGS TGCCAGGAGG GCTTGAATCA GACCCCTGTC
    TGTCTCTCCC GAGGACACCS ACGGTCCTCC CGAACTGAGT CTGGGGGACG
-1 -----
```

FIGURE 2C

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+1 -----  
PstI  
~~  
1201 AGCTCAAGCA TGTYTGCAGG ACACCCTGGT CCCYTYTCCA YTGGCWTCCA  
TCGAGTTCGT ACARACGTCC TGTGGGACCA GGRARAGGT RACCGWAGGT  
-1 -----  
  
+1 ----->  
1251 GACATCTGCT TTGGGTCATC CACATCTGTG GGTNGGCCGT GGGTAGAGGG  
CTGTAGACGA AACCCAGTAG GTGTAGACAC CCANCCGGCA CCCATCTCCC  
-1 -----  
  
1301 ACCCACAGGC GTGGACAGGG CATCTCTCTC CATCAAGCAA AGCAGCATGG  
TGGGTGTCCG CACCTGTCCC GTAGAGAGAG GTAGTTCGTT TCGTCGTACC  
-1 -----[  
  
1351 GGGGCCTTGC CGTAAACGGG AGGCGNGACG TTGGCCC  
CCCCGGAACG GCATTGCCCC TCCGCNCTGC AACCGGG
```

FIGURE 3

1 MHYYRYSNAK VSCWYKYLLE SYNIIFWLAG VVFLGVGLWA WSEKGVLSDL
51 TKVTRMHGID PVVLVLMVG V MFTLG FAGC VGALRENICL LNFFCGTIVL
101 IFFLELAVAV LAFLFQDWVR DRFREFFESN IKS YRDDIDL QNLIDSLQKA
151 NQCCGAYGPE DWDLVNRYFNC SGASYSREKC GVPFSCCVPD PAQKVNTQC
201 GYDVRIQLKS KWDESIFTKG CIQALESWLP RNIYIVAGVF IAISLLQIFG
251 IFLARTLISD IEAVKAGHHF

FIGURE 4

NTSP5:P104	CHIR22-1	TGCAGCCTTTCGTGAAGATGGACTC	25 (7-11-7)
NTSP5:P727	CHIR22-2	CCCCATGCTGCTTTGCTTGATGGAG	25 (7-11-7)
NTSP5:P285	CHIR22-3	GCTCAGCTCGGCTCCCTCAACTC	23 (7-9-7)
NTSP5:P456	CHIR22-4	CACAAGTTTGGGCAGGTAACAAGGG	25 (7-11-7)
NTSP5:P395	CHIR22-5	AGAGGTCACGTCACGCTGATGCTTA	25 (7-11-7)
NTSP5:P104	CHIR22-1RC	CTCAGGTAGAAGTGCTTCCGACGT	25 (7-11-7)
NTSP5:P727	CHIR22-2RC	GAGGTAGTTCGTTTCGTCTGTAACCC	25 (7-11-7)
NTSP5:P285	CHIR22-3RC	CTCAACTCCCTCGGCTCGACTCG	23 (7-9-7)
NTSP5:P456	CHIR22-4RC	GGGAACAATGGACGGGTTTGAACAC	25 (7-11-7)
NTSP5:P395	CHIR22-5RC	ATTCGTAGTCGCACTACGCTGGAGA	25 (7-11-7)

FIGURE 5

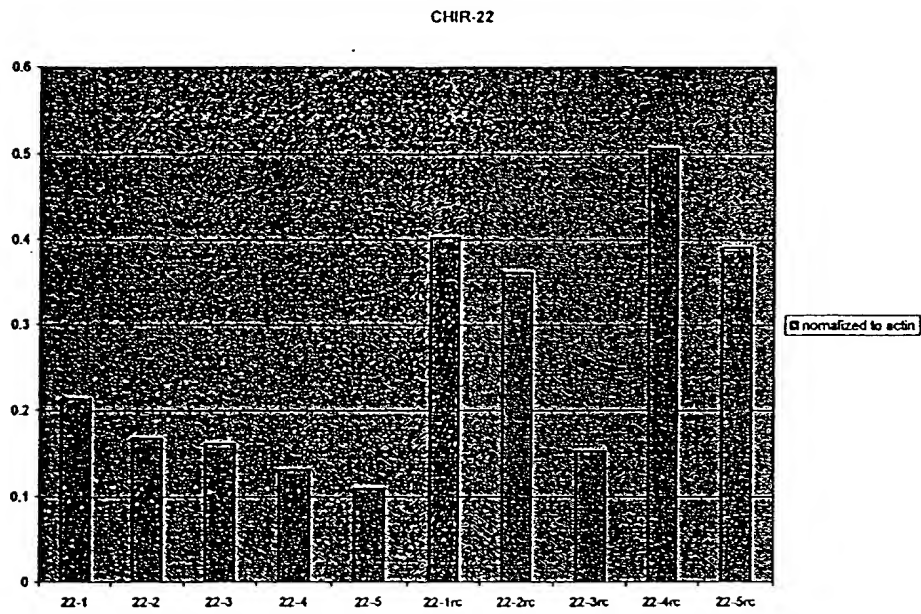


FIGURE 6

